

Fig. 1

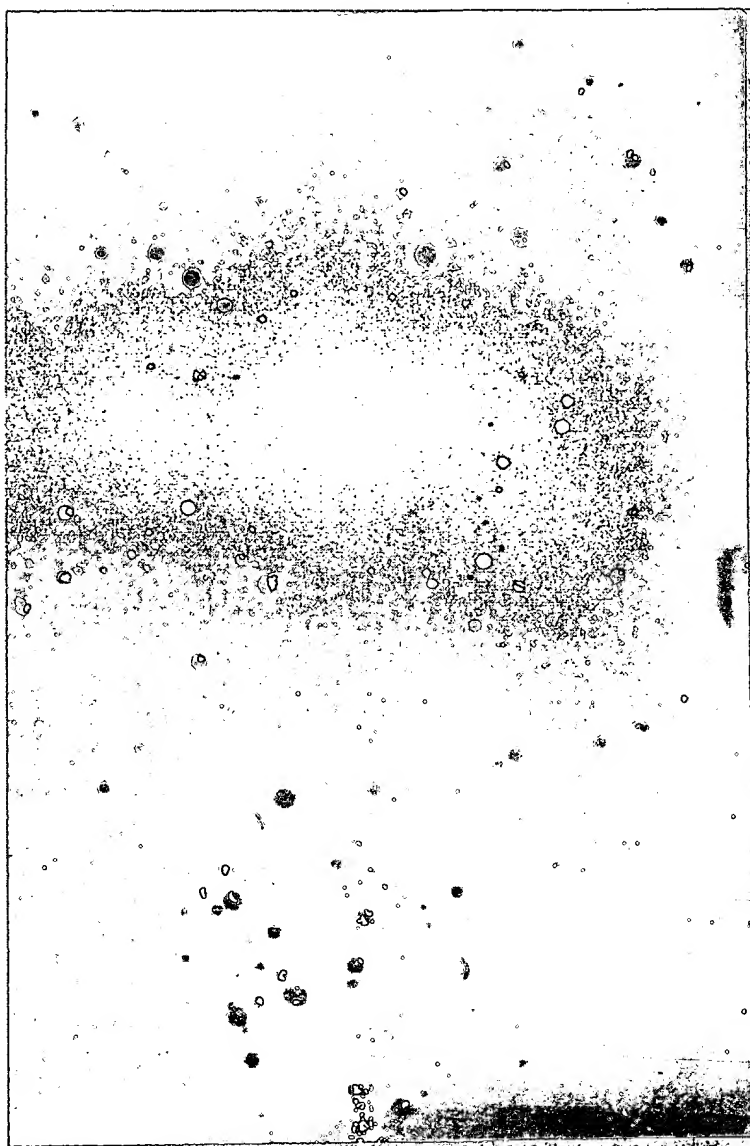


Fig. 2

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11:11 AM
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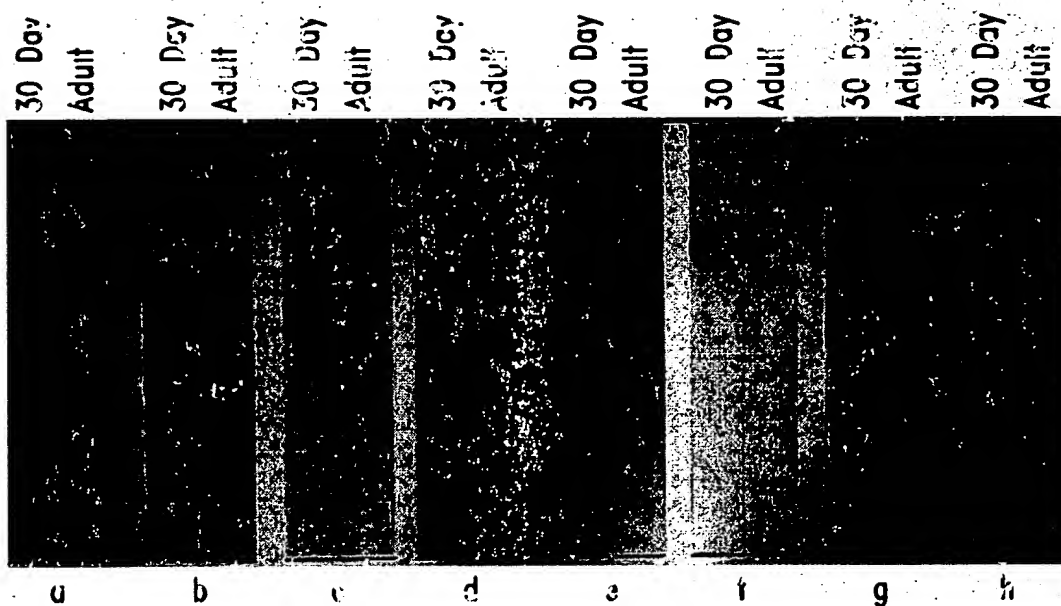


Fig. 3

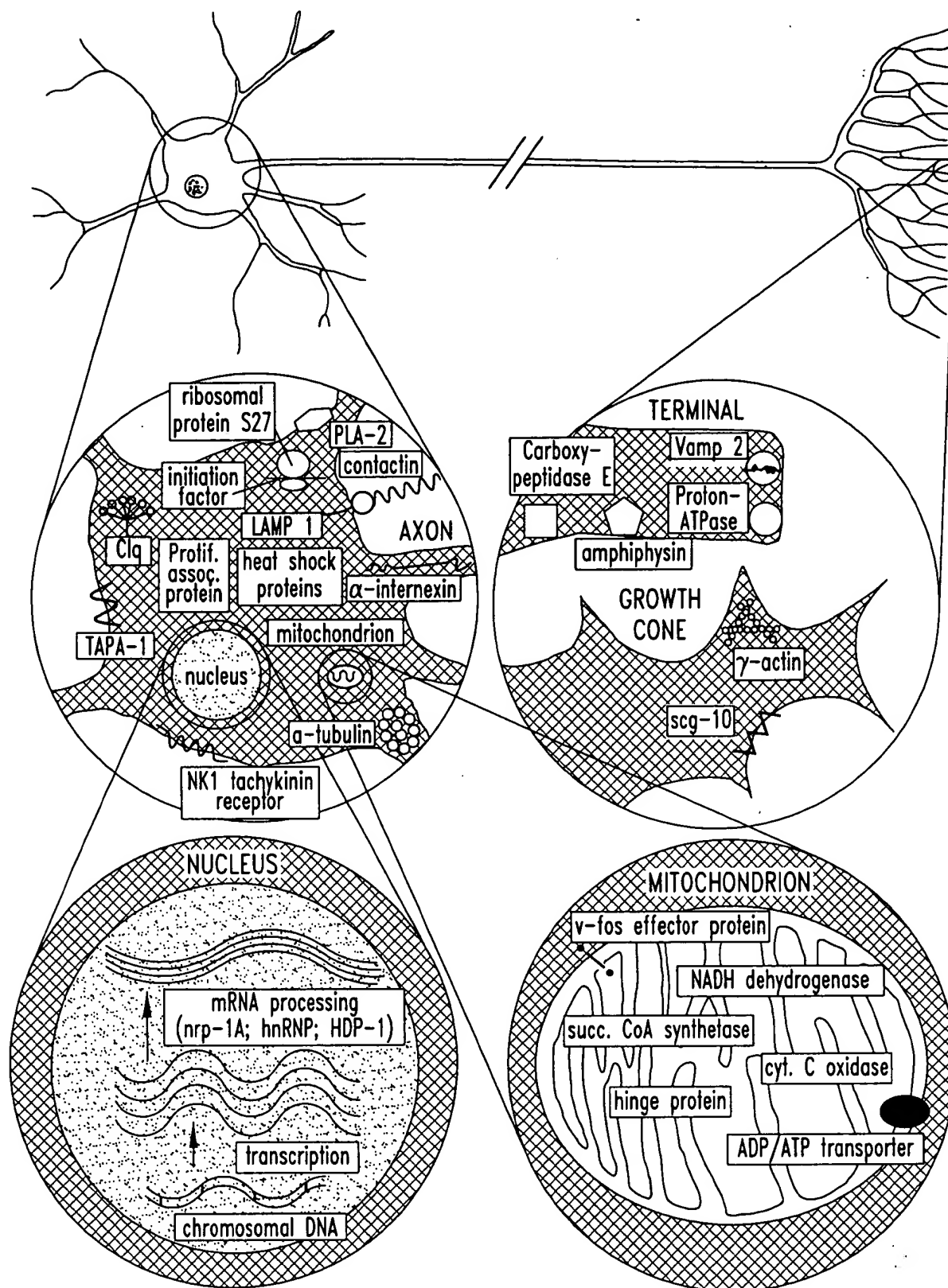


Fig. 4

SEQ ID. NO.: 1

pKVC43:

CCTGGCTGCCTGTGCCTCAACCCCACTCCCAGGGAGACCAAAAGCCTTCATACATCTGAA AT

SEQ ID. NO.: 2

pKVC2B:

GCGACGGACGAGATGTCTTCGGTGTCTTGCCTTCGCTACCAGGTCAAAATGCAAATCTTCGTGAAAAC
CCTGACgGGCAAGACCATCACCC

SEQ ID. NO.: 3

pKVC15:

TTTTTTTTTAATTGAGAAAGACATAATGGTTATGGCATTGGCTTGAAACCAGTTAAACACCGTTTCGATT
CCTTCCTTTCTTATTTTAATAGTACGTtAAGTTGGCTCTTCAAAT

SEQ. ID. NO.: 4

>pKVC24BR

poly(T)ATCCATACTTGCTATTTATTTAGGCTTCTAGTTTGAACAAAAGGNCAAGAGTTAAAAAAT
GCCAACATTTCAAGGACCCTTGTT

SEQ ID. NO.: 5

pKVC26B:

CTTCCCCCACTCATCCCTGCTCTGGTCCCTTGTgCCCCCTTGGCCCTTTACCCCAAGCACCACCCACAG
ACTGGGGACCAGCCCCCTCTCCTGCCTATGTCTCgCCCCAAAT

SEQ ID. NO.: 6

pKVC50B:

CCTTCCCTTCCTTACTTTAATAGTTCGGTAGTACGGANGTTAAATCTTCAGGTCGGTGGTACGCAGCCG
GGCAACCATGCAATGGATTNAAGGTNGGTAATGGTACAATTGGCCTATGCCCACTTT

SEQ ID. NO.: 7

pKVC85B:

CTTTAGAGCGCACTCAGGGGCACTTGNAAGGGCTTCTCACGAGCGTGGCTGTGGCCATCTGTGGAAAGA
GCTTCTCGCAGTGNTCGGTNGNNTTATCCCCACGCCCNTAGNGCACTACTC

SEQ ID. NO.: 8

pKVC100:

TTAGTTTCACATTCAAGGGGCTTATGAAGAGATGCAAGTCAGGATACATAGGCTTGATTC
TTGGCAGCTTAaTGAGTaTTCACtGAGGCACTtG

SEQ ID. NO.: 9

pKVC94B:

CCGCTGATATAGACACTTCGTAGAGCGTAGTTTGACTATTCTATACGTTTCTATTTATTGATGAGGA
TCCTAAA

SEQ ID. NO.: 10

pKVC90B:

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TGTTTGGCATTATTTATTNNTTATAAATATATATTTTTCTGAATGTGTCCTGAGNTCCAAAGAGGTTGGG
GGNGGGGGNG

SEQ ID. NO.: 11

pKVC91B:

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TTTTTCCAACACACAAACATAAAAAATAAAAACAAGTCGGACCGCTACTTCTGTGTAAATCAAGATCNTT
GGGGAA

SEQ ID. NO.: 12

pKVC101B:

CCTGGCCAGCGGGCAGGGCCACGAAGGCAAGATCGGTGCTTGTGCTTGTGTTTTCCAAGGAGACGANCC
NATNANCTGTAAATATGTACACGTNTCTGTCTGTGTGTCCTTCGNGGNAGG
ATGGTCGGNTCTATTTAAA

SEQ ID. NO.: 13

pKVC103fB:

CCAAAATATATTTGGGCCAAATGTTCCGAGGATGAGTCAGGCTGTCCTTCGCGCGGGCGAGACGAAGCT
TCACACGGGACAAGATGGGATGGGTGGAGGAATGGATGGTCCCCAAACA
ATGGGCTTANAANAATTAT

SEQ ID. NO.: 14

pKVC105:

TTTACTGACAAGCATGGGGAAGTGTGCCAGCTGGCTGGAAGCTGGCAGTGATACCATCAAGCCTGATG
TCcAGAAGAGCAAAGAATATTTCTCTAAGCAGAAGTGAGCGCTAGGCCTTTT

SEQ ID. NO.: 15

pKVC107:

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ATACTTTACATCAGCCACTATAATTATTGCCATTcTACCGGGGTGAAAGT ATTTAGTTGACT

SEQ ID. NO.: 16

pKVC1B:

GGAGCTTGAAGAAGAAGTTTTTTACCACCGTCTTTTTCTACTTTATACAGAAGTAGATATTCCTGCGAA
GAAGAATAATTTGGGGTAATATGCAAGCTAGTAGATGTGGCACAGCAAATC ATATAATAAA

SEQ ID. NO.: 17

pKVC5B:

ACCCACCCAGAGCCTGGAATCAGGATCCCAGGGTCTAGCCAGCCTGGGGTCCAGAACCCAGAATCCAG
CCTGTCTGAGCTGGACCTAGCAGCCCAGAGTCTAGCCAGCCTCGCTCCAAGAGGGGCTCTGGTGGCCTA
GGTAGACAGGCCTGgTGGGGATCAATGAGTTGGTGCTAGGGCCAGGGCACCTCGACTCTGCTCCATAC
TG

Fig. 5B

SEQ ID. NO.: 18

pKVC7:

CACCTTCCTGAAACACCTGTGGCTTTGACTTTGTTATTGATCCAGATTATTCTCCTTGCAATTGGGGAAA
ATATCTTTCATATTTCACTGTAAGGGATGGTTTTGCGAGAGTAAGTTAATGTCAAGACAACTGCCAAT
ACAAGAGCCCAATGATATTAATTACATGAGAAAAaGTAAC TAACATCC

SEQ. ID. NO.: 19

>pkvc55R

GAGAAAGAAAGAGATGTTTTATTAGCATTTGTTACAGCAACGgTGACGTGAAGGGTCGTCCGTGCACAG
CCACCCGAGCGGCAAGGCGTAGGCCAGAGCTGACACCCAGTATTTACACGAGTGCAGAACAGGATCACC
CCGAACCTCAAACAGAAGACTGAAAGTCACTTTACAAAAAGGTAAATAAAAA

SEQ ID. NO.: 20

pKVC13B:

GCTACGGTCGACATCACCATCTTTATCCCTTCAGCCCTTTGCTGGGTCGCGGGCCTTGGAAGATGCC
AAAGAGCCGAGCAGTGGTGGTGGCCAGCGGGCAGAGTGTCCCTGCTTGGGCCAGGAAAGCTTTACCTTC
TCTGAGCGCCTCTGCCTGAGAGATCGATGGTCTGTGGCTCTA GGAGACCACGTCTTGGAGTG

SEQ. ID. NO.: 21

>pKVC6R

poly(T)CCTTCTTTATTGAATGACTTTCAAGAgGTAATTACAGTTGAAGGTGACAAGTTAGAAAGGAG
AGGTGCCACTGAAGGCATAAGGCTGCTTGTAGACCCGGCTCTAGACAAGTGGCAGGAGAAGAAAGAGGG
TTAAAAAAGGCATGAGCGTGCAGCCACGGGGCA

SEQ ID. NO.: 22

pKVC16B:

GGCAGCACTCCTATTAACCTGGAACCTACTGAGGTTTCTCGTGTAATTAGGGAACAGAGAAACACgt
tCCACGAGGGAGCCTCCAGGTCTAATTACCTGCAACCTCGCTGTACCTTGCTGGCGAGGAGGGAGCCAC
CAATAGCAATTACTAACGAATGGCTGAATTTCTTATAAGACCTAGGGAACCTGATGGGAACTGAATT
GCTAA

SEQ. ID. NO.: 23

>pKVC74F

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GGAGGGGCAGAGAGAGAGGGAGACACAGAATCGGAAGCATGCTCCAGGCTCTGAGCCCATCAGCCCAGA
GCCCGACGCGGGCTCGAACTCACGGACTGTGAGATCGTGACCTGAGCCGAAGTCAGACGCCCAACCAAC
TGAGCCACCCAGGCGCACCATC

SEQ ID. NO.: 24

pKVC29B:

CCAGGTGACAGGGAGCCTGCAGGGAGGGTCTGGGTGTTCCAGGAGCCAGGGGAAGTGGGAATGGTGCA
GGCAGTATTGGAAGGAAGGCCAGTCAGTGGGACTGGCAGCTCAGACAGGCAATATGGGGAAGCATTGGA
GCTTGCACTCTCCACTCTGGGGTTAGGGGTTTGCACACTCAGCAATAAATAACTGTGTACACCAAATC
CTAAATATATCACTACAAA

Fig. 5C

SEQ. ID. NO.: 25

>pKVC79R

poly(T)GTGTAAAGTGGTCTTTATTGGGGTGTCACATTAGGTTATCTTCTTCATTATCAGTTCTTCAG
TTAATTGTACAAGTATGATAAGTTATTTTATATCTGACGTGGGAATTTAAATGTAAAATAAATACAAAA
TACATCTGTGGTTTAATGAACACTCAATGAAGAC

SEQ ID. NO.: 26

pKVC30:

ACAACAACCTGTTGCAGGTGCTTTTGTGTGGAGTGTGTGGATCTGTTGGTGGGGCCGGGGGGCCAGGAC
TCAAGGAGGACCCCTGGAAGTGTACATGTGCGGGCACAAGGGCACCTACGGGCTGCTGCGGCGGCGGG
ACGACTGGCCCTCGCGGCTGCAGATGTTCTTTGCCAATAACCACGACCAGGAGTTTGACCCTCCGAAGT
TTACCCA

SEQ. ID. NO.: 27

>pKVC7R

poly(T)ACACAGAACAAGAAATTTTATTATCTCGAATGCTGGTGCATAAGCAATAACAAGCTCATCAA
TTAGAGGAGGAGACAGAGGGAACTTCAGATACTGATGAGGATTTCTGGGCAGGTTTAAACCTTTAA
GATTGAGGCCATAATTGTCAGTCTTTTTTT

SEQ ID. NO.: 28

pKVC32B:

CCTTGCCAAGGCCGAGGCTCCACAGGAATCAGAGTTGGGACGACNNNNGAAGGAAGCGTTTGGCTTCAC
ATTCTAGAGAAAGAAGACCCTACTGGGCTGCAGACCCCTCCAGGGCTGTAGGAAAGCTGCTGGACCTCT
TCTGCTTCTCCCCAACCCTCTGCCACTCTGCCAGTTACCAG TCACCAG

SEQ. ID NO.: 29

>pKVC45BR

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ATTTTGCTTGCAAGAAAAATACTCCAGATTCATTTTAATGAGAATCTTTGAAATGTATTTATCTTTAGG
GCATTTGGGGCACTTTAATGCCTGTTGGCCTCCGGCCTTCTGGAAATAAAAGGTCCAACGG

SEQ ID. NO.: 30

pKVC34B:

CCTGCCCCACGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACCTGACGGACTACCTCATGAAGATCCT
CACAGAGCGCGGCTACAGCTTACCACCACCGCCGAGCGGAAATTGTGCGTGACATCAAGGAGAAGCTC
TGCTACGTGGCCTTGACTTCGAGCAGGAGATGGCCACCGCCGCTCCTCGTCCTCCTGGAGAAGAGCT
ACGAGCTGCCCCGAC

SEQ. ID. NO.: 31

>pKVC89BF

ATTGTGATAGAAGACCACGGTGGGTTCAANCANGTTGAAGNAGTTCCGCNTTCCCTCCGGGGGAAAG
GTTGTGATGTCTNTTGGTNNTAAGTANTACCCATNCATTGTTGACAAGGNTCANTCCGAAGGGTCA
TTCTTGAGTAGTAGACCAATATTNTAAAAATAATTTNAATCCTT

Fig. 5D

SEQ ID. NO.: 32

pKVC34:

AATTGAGAAAGACATAATGGTTATGGCATTGGCTTGAAACCAGTTAAAGAGGGTTCGATTCCTTCCTTT
CTTATTTTAAATAGTACGTAAGTTGGCTCTTCAAATGTGTGGTACGGAGGAGGACATCCATGCAATCATT
CAAGATTAGTTGTGGTTAATTCTACTATGGCCACTTCTCGCTTGGATGCGAAAGCTTCTCACACTATGA
AAA

SEQ ID. NO.: 33

pKVC36B:

ACGCTCGTTTTCCAAAGAGAAGAGCGTTGTTTAGAGTAGCGAAATTCGAAGGCTGCTTAGGCGCATTGT
AAAGCTGTTGGGGAAATAACTCCACAAGTTTCGTGAGTGGAATGTAGTGCTCGAAACACATTCTGCTT
TAAAAGGTTGTAACAAATACAAACAAATTTAAAAAAGCTCT CGAAAA

SEQ ID. NO.: 34

pKVC43rB:

CTGGAGCGCAAGTACTCCGTGTGGATCGGTGGCTCCATCCCGGGCTTGGTGTCCACCTTCACAAGTG
TTGATCACACAAGCCGGAGTACGCGCGCGGTTCCGGCCCCCTTCATAGGCCACCGCAAAAACTTTtaggc
GGGCTCTTACNTTAGAGGCGGTACACACCTTCTTG

SEQ ID. NO.: 35

pKVC73:

TGGGCATCAAATGAAAGAGATACTTGCAAAGGCTCTTGAGGGGCAGGGAAAGGAAAGGAGGACTGTCTG
CTTTGGACCCTAAACTGGACAGGGACTAGGTATTTTTGATGTTTCATAAGTTGTCCTGCTCTAAGTTTCT
TTGAGTAGCAGACCTGACAAGCATTTGAGGTCAAAACCTACCATGTGTAAAAAAAAA

SEQ ID. NO.: 36

pKVC79B:

GTCTTGATACAAAGCTTCTGTGCTAATCCAGACTATTTAGGCAGGGGCAATAGGGTGTAATGTATCT
GCTCTCTTCAAACGCGGCTAANGNTCTAGTCCATGTCCNCCNNGCAACCNCAANATCCCACNAGGGG
GNAGNTCG

SEQ ID. NO.: 37

pKVC81B:

CCCAGGTGAACAGGAACAGGTTTTCTCATAAAAACAACAAAAATCCTTGCCATTATTTTCTTACTT
GNATGTGGAAAAATAGATCCGCCTTTATTGNTGAATAGCCTTAAACTTTTGGAGAATATTCCTTAGNA
AATTAGGGGGGNGGGGC

SEQ ID. NO.: 38

pKVC83B:

CATCTAGATANTCTTGNGATTGGGGCCTCTAGNTGATTGCTCGAGCGGCCGCCAGTGTGTTTTAAAGA
CTGGCTCAGGGCCTGTGCGAGGTGCTGCTGGTGGTGACCAAGGAGGTGGAGGAAAAGGGCTGCTGGNCT
GCGGNACAGTACTGACCCCGCGGAGGTAGTAGCAACCAGGTCCACCGTACCCCTGCGAGTCCCCCGCTG
CCAATCCCC

SEQ ID. NO.: 39

pKVC87B:

CCACCAAGAAGCTGGACCTGTGGATGCTGCCTGAGACACTCATTATCCACCTGAAGCGCTTCTCTTACA
CCAAGTTCTCCCGCGAGAAGCTGGATACCCTTGTGGAGTTTCCCATCCGGGACCTGGAACCTCTCCGAG
TTTGGCATCAAGTCCGTAGGAACGAGTCGGCTCCGGAGCTGTACAAATACGCATCTCATCGNNGGNTNC
CATCNCATTNATGGGGG

SEQ ID. NO.: 40

pKVC104fB:

GGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGGCGCCAGTGTGCTCTAAAGCCAAAATATATTTGA
GCCAAATGTTCCGAGGATGAGTCAGGCTGTCTTCGGGGGCAGNAAAGGCTTCACACGGGACAAGTGGAT
GGNTTGGAGGAATGNATGNTCCGCAACCATGGGCT

SEQ ID. NO.: 41

pKVC104:

CTGACTGGCCCAGAATTTTTGAATACTGGAGGCAGTCTCATTGGCCTCCCTCATTAGACTCCAGGATTCT
GGTCCAGCCCCGAGACCACTGTGGGCTCCTACCAGTCCAAAAGTCTAGGACCGCTTGCAGACCCAGGAAA
GGAATTTTCTAGTGTTCTACAAAGGCCAATAGAGAGGGTGGGAGTGGGTGGGTGAGGACCGGTGGCGA
GAGGGG

SEQ ID. NO.: 42

pKVC109B:

GCCAGATTTACATAAGAACATGCTTAACAGACGATCTTTTAGCTGACGTCTTACCAGNAATCGCCCAAG
TCCGCACGGTAAGTAAAGAGGAGGCCCGCCAGGTGAGAGTTTGCTTAGCAATAGGGTCAGGTCATAAA
ACTGTAAATCCATTGCGAGAGGGGGACGCCTCCGCTCAAGCT TGGCTGGGCTTCGGC

SEQ ID. NO.: 43

pKVC89B:

GTCAAAGAGACCAAATCCCATATCCTCATCTGATTCTCCGACTCTTCCTTTGCTTCAACCTTGGCTGG
GGCTGCAGCAGCAGCAGGTGCAGCAGTGGTGGCAGCGGCCACGGGGGCAGCAGCCACAAATGCAGATGG
GATCAGCCAAGAAGGCCTTGACCTTTTCAGGCAAGTGGGGAAGGTATAATCAGGTCTCCACAGGACAA
AGGCCAGGACCCGCTTATTTTCCATTGGATGGATAGGAATGGGGGGCACTGNATGCAAACAGGNCGGGG
TTNACCCTTTCTTGNAGGACCATT
TCA

SEQ ID. NO.: 44

pKVC115:

GCGCAGGCACAGCTGGTGAGGGGGCGAGGCCGAGACGCCAAGGTGGCCACCATGGTCCGGAGTGCCTGC
AGGTAGTGGGCTTCGTACGAGCTTCGTGGGTGGATCGGCATCATCGTCACCACGTCCACCAACGACT
GGGTGGTGACCTGCGGCTACACCATCCCCACCTGCCGAAGCTGGACGAAGTGGGCTCCAAGGGGCTGT
GGGCAGACTC

SEQ ID. NO.: 45

pKVC20fB:

CAAACCCATGCATACCACATAGTCAACCCTAGCCCATGGCCACTTACAGGAGCCCTTtCAGCCCTCTTA
ATAACCTCAGGCCTGGCTATATGATTCCACTACAACCTCAACACTGCTGTAAACCCTTGGAATAACTACC
AACCTACTAACTATATATCAATGATGACGAGACATTATCcGAGAAAGCACATTCCAAGGCCATCATACA
CCTATCGTTCAAAAAGG

SEQ ID. NO.: 46

pKVC7B:

GCGCCCGCCGCGTCGCGCCGCTCACC GCCGTACCACCCGCCGCTCCTCTGCAACCTCAGCCCACCGG
GGCACCCGGCCAGGTCACTGGCGGCCAGGCGCAGCTCCTGGAGGAGAATGACCAGCTCATCCGCTGT
ATCGTGGAGTATCAGAACAAAGGCCGGGCGAATGAGTGCGTCCAGTACCAGCATGTGTTACACAGAAAT
CTCATTTATTTGGCTACCATCGCAGATGCCAACCC

SEQ ID. NO.: 47

pKVC92:

AGACCAGCCGGTGACAACCACTAATCAAGTTCCATAACTATATAGCGCCGCAATTCCCATGGCCTCCTC
ACTAAAGAACCCCTGAGTCACCTGTATCATAAATCACCCAATCACCTGCACCGTTAACTTAAATACGAC
TTCTACCTCATCTTCCTTTAAATATAACAAGCAGTTAATAATTCTGCTAACACCCCCGTAATAAACAT
TGCTAGTA

SEQ ID. NO.: 48

pKVC8:

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GATTTAAATAGATTGTTCACTTTTAAATATTAGCCATAGAACTGGTTAGTATCTCAGTAGTTTCATGAA
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AAGTTTGTAGATTTTAATAAGCAACAATTTTAAAGATGCGGTAATCTTCCAATAATTTTATCCATC
TTTCATGGCCCCACAACCTGCATCTTTAAT

SEQ ID. NO.: 49

pKVC8B:

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ATCAACAGCAAGGTCTACTTCACATGGCCACTCCAGTCCTTTGAGCTATAATCAGGATTATATAACTTA
CCCTCAAATCAAAAGTTAAGAAAAAGGAAGCCATAAGCTAAGGCACTGAATCTTTTCCTGACAATTTT
TAGAGGTAGAATTTTCATCATGCTGCAGAGAGAGAGAGAGAGAGAGAGAAGGAGGGGAGGGAAG
AGAAATGAAAGAG

SEQ ID. NO.: 50

pKVC14:

ATAATGGTTATGGCATTGGCTTGAAACCAGTTAAAGAGGGTTCGATTCCTTCCTTTCTTATTTTAATAG
TACGTAAGTTGGCTCTTCAAATGTGTGGTACGGAGGAGGACATCCATGCAATCATTCAAGATTAGTTGT
GGTTAATTCTACTATGGCCACTTCTCGCTTGGATGCGAAAGCTTCTCACACTATGAAAACATTAACAT
GACTGCTGTTAATGAGATGAAAGAGCCCATTGAGGAAATCGTATTTCAAGTTGTATATGCATCTGGATA
GTCAGAATAAC

SEQ ID. NO.: 51

pKVC16:

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ACAAGCTTAGCAAGTTGATCAGGATAGGGTTATTTGGTGGATAGACCATGAGTGTCAGGGACCTCCCAC
TGGACACCACCCAGAGGCTCAGGATGCTTTTCGAGGGAGGAAAGGAGAAAGACCTCTACTGAGGGAAC
AGCTGGCCGTGTGTGGTGGGCTGAGGTGACGTACAGGGGCAGAGCTTTCGAGGGATTTTCAGATGATCC

SEQ ID. NO.: 52

pKVC20rB:

TAAATAGAAACGTATAGAATAGTCAAACCTACGTCTACGAAAGTGTCATATCAGGCGGCGGCTTCAAATC
CGAAGTGGTGATTTGATGTAAAGTGATATTTTAGTTGGCGTAAGAAGCATACAATTAGGAAAGTAGAGC
CAATAATTACATGTAGCCCATGGAATCCTGTGGCCATGAAGAAGGTAGATCCGTATACTCCGTCCGAGA
TCGTGAATGATGTTTCATAGTATTCTGGAGGCTTGAAGGAGTGTAAGTAGACTCCTAAAGAGATTGTA
ATAAATAGTGCTTGAAG

SEQ. ID. NO.: 53

>pKVC59BR

poly(T)GTTTTTGTGTTTTAAAAATGAGTTCCTTTTAAAACCATGTCATACATTCCCCATACTGATATCG
CATGACCCNTTANAATAAAGGCAGGGGNTTTACTAATGGGGGGCGGGCCANACCCNCCATCGTTTTCA
GCCAGACAGTTCAACCCGGGGNNCCTTGTTCTGCGGACCTCCGGGGNANGCCTTTCCTTTTCCAAAAA
GGGGGCCGNTCGGAGNATGNATNTNGAGGGCCCAATTAG

SEQ ID. NO.: 54

pKVC21B:

GCGCTCTGACCAGGCATCAGTTTTCTGGTGCTCTCTGGGCTAGCCTGGTGATGTAGGGCCAGGCAGAC
AGGCAGGCAGGGGCTGAACAGGGTTTTCTCTGCTCCAGGAAGACCAAAACACAGAGGACCTTACAGGCAGG
AACCCACAGACTGTCCCAACCCACACACTCCACCACCTGTGCCCTGTCCCATGTCTGAGCCAAGGCC
TGAGGTAGAAAGTCACCTGATCCTGTATCTCCATAGGGGCCTGACTTT

SEQ. ID. NO.: 55

>pKVC61BF

poly(T)CCCNAGNGCACACNGGNGGCCNTAANNAGNGGNTCCNAGCNCGGNACCNAGNTTGAGGCATA
GCTTNAGNATTCNATAGTGNANCACAAATAGCNTGGGGNAATCANGGNCAAAGCCNTTCCCGTGNGAA
ATTGTNATCCNNTCANAATTCNCACAAANATACGGGGCCNGAAGCATAAAGNGTAAAGCCGGGGGGCCC
AANGNGGGNGCNAACTCACATTTAATNGCG

SEQ ID. NO.: 56

pKVC23:

GGGAAATGTAGTTTGGATGCAAAGCTGATTAAATTGGATCAAGAAAAATTGGAATTAATACATACAAT
AATGCATGCATTTATGGTTTCGATTTTTATATATCCTTAGCTAGTTGGAAATGATGATTCCACAACAA
GCATAACTCAGCTTGTTTCTGCTTACTGAGTACTTCTCCTATGGTATATGTTGATAACATTTCTTCCA
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SEQ. ID. NO.: 57

>pKVC9R

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CTTTAGCACCGGTCTCATCCCAGTAGCTTTTCCAGAACTGCTACCTTCACCATGAAGCTCCATGAGCT
TTCCCAATTCAAACCTTGGGCTTCTTCAGCATTTTTACTTTTCTAACGAAGTCATCATGAAGTGGATAAA
TAGACTGACAAGCCTTCTCTATGTCTTTCCGATCTGTCTGGAATCAATTTATTGACAACCTTCTTCAA
GTCA

SEQ ID. NO.: 58

pKVC28B:

TCATAGCATTTCTTCTGCTTCTCCTGGATTATGTGCTACAAATGTGCTTTGGCTTTAGAAAGGGATGGA
TGAGAAGACAGAGCTGAGATCAACCTGGGTAGAAGCAGAAAGTTAAACCTTTAAAAGTGCTGAACACA
GATTCGAATCCAAATGGTTCAAGCAGCCATGAAATCGCTCTTCATGAAGTGGGCTTAATTCTCTAGTTT
AAGTTCTTTTGATGGAATGAATTAATTAATGTGTGTCAGGTGGCTTATTTGTGGATGCATGATTGATGATG
TCATT

SEQ ID. NO.: 59

pKVC29:

CGGACCCGGACAGAAAGCAAATCCTGGAGCGCACCCAGCGTGCGGTGGGGCTGGCCGACAGAGCCCCTGG
AGAGAGCCGTGCGGgNCGGCCTCCCGGCAGAGGAGGCCGCCCGCTGCGCAGAGGTGTTGTTGGAAGAAG
CGAAAGATTTGCTCTCCGACTGGTTGGACTCCACCCTGGGCAGCGAAGTTACGGACAATTCTATTTTCT
CCAAACTGCCCAAGTTCTGGGAAGAAGAATTCCACAGAGACATGGAAACCCTGAACGTTCTCCCTCCGG
ACGTCCT

SEQ ID. NO.: 60

pKVC38:

CGAATCTGTTGTAGCAGTTTCAAATGATTGTGTGGATATTGGATGTTTAACCTTTACCATTTGCTTTGT
ATCGACACATTTTTCATTTTAAGTGTTAACTCATGTACTGTTTACTTTAGGAATAATGCAAATCCAACC
TTCATCCAGTGATGAGAATAGCAGTATGATAGGAATTTGCTCAATGTGCTTTAAATGAGTAATTGCTTT
ATCTTTTTTAGTATCTGATAGACTTTGCATGACACGGTACACTCCTAATTATGCATTCTTTAGTTTCCA
AATCTTAACCTAAGACATTCTATATTAAGTATGATGGGTAGCTGAG

SEQ ID. NO.: 61

pKVC48B:

GGTTTTGCAGGGGCAAGTGGGGCTGGGCCCCGCTGGGTGAGAACCCCGCCGCACACTGCAGTGGGTGCC
TGGACCCCGCAGCAGCGCTGAGCAGACGGTGGACTCTGGGCTGTGGCCTTTCTTGGGGCCACTGGGGCC
GGCTCTTGATATAGCTGGGGCTCATGGGCATGACCCCTTTTTTAAACCTTGGGTCTTAGGACACCTG
GGTTTACCCTCAACTAAGGGAGGGTGGGAAAGGGATTTACTTGGGGTCTCAATAATTTACGATATCCCT
TTAAGGTTGACCATTAACCTGTCCCA

SEQ ID. NO.: 62

pKVC51B:

CCTCTTAATAACCTCAGGCCTGGCTATATGATTCCACTACAACCTCAACACTGCTGTTAACCCCTTGAAT
AACTACCAACCTACTAATATATCAATGATGACGAGACATTATCCGAGAAAGCACATTCCAAGGCCA
TCATACACCTATCGTTCAAAAAGGCCTTCGATACGGAATAATCCTCTTTATCATCTCAGAGGTATTCTT
TTTCGCAGGCTTTCTTCTGGGCCCTTGTTACCACTCAAGCCTAGCCCCAACCCCCGTAGCTTAGGGGG

SEQ ID. NO.: 63

pKVC53B:

SEQ ID. NO.: 69

pKVC69:

TGGCTGTCATCTGGAGGCTTCTGCCTCAGCTCCTGAAGGCTGCTCTCATTCTTCTCGCGTGCTCCCGT
CCATCTTCAAATTCTCAATGGCCCATCTTCTCAGCCTCCCATCCCTCTGCCTTCTTCTCTGTTTTAA
GGTTCATGTGATTAGATCAAGCCCACTGATCAAGTCTCCCTATTTTAAGGTCAGTTCTGCCATAGAACA
TAACATAATCACAGGAGTGACTGCACAGGCACGGGTTCTGGGATTTGGGCATGGAGTTGGGGG

SEQ ID. NO.: 70

pKVC74:

ACGCTAAGGACACCTTTTTTGTCTGACCTGATGTTATAGATGGCAACACCAAGTTCTAGAGCAATT
GAGAGACTTGTCGAAGGTCACAGGATGGCTTCACTTCAGCCAACCTATATAGTTGCAGTGACAGTATGTG
TGCTCTCTGAGGGGTACTGAAAACCCCTGTCAAATATTTCTGTGGACACTCAGCCTTTAACTCCCA
AGCCTCATGAAGAACTTATTGGGGGGGGGGGCGCCTAAATAATTCAGTCGGTTGAGCGTCTGACTTCG
GCTCAGGTCATGATCTCACAGCTC GTGAGTTCGAG

SEQ ID. NO.: 71

pKVC86:

TGCCTAGAATCATTGTTCTGTGTGGAGGTGTTTTGTTTTGATAGAAACCGGCCAGTCTTGAACCAGAAC
GAATGTTTCCCTTGTTCTAATGTTCTCACAGAGAAATGGACAAGCGTTTTACAGGTATAAAGGCACAAG
GAGGAACCTATTTTTGGTCAGAGCATTGGGGAAGTAAATCACAAGGCAAAATAGATCTGTTTGTGTTT
GTTGCGGGAGGAAGTATTAATAAGCAAATCAAATGCCTTGATGATCTCCAGTGTTATAATTATAGATC
CTAACTTTGCAAATACATGTAG

SEQ ID. NO.: 72

pKVC96B:

ACTGGACCAAAATTGGTGTGTTGTTTAACTTGACTCTTCTTTTGATTATTTCTAATGCTACAAGAATG
CTGTAAAGTGCTTCTACAATGATGTAGCCCTGACAAGACATGTTTGCCAGTGTATAAAAATTAGGTAG
GATTGTGCACTGATTGACCATTTGTGAAATCTTTTCTCAGTGGTAAGTGCATTCTTAATAAAATTTAT
GNAGGTGAAACAATCTTTGGNGCAATGGACCACTCATGCATCCATCCC

SEQ ID. NO.: 73

pKVC97B:

AACAGCCCCACTATCAGCACCCAAAGCTGAAATCTTTCTTAACTATTCCTTGCCAATACCAGNAAAG
CAACCCCATAACTTTCATAATTCATATATTGCATATACCCATACTGTGGCTTGCCAGTATGTCCTTAT
TTCCACAAAAAACCAAGTAANAAACCCCAAGTACCACAACCAAAACACACAATGTAAATCACTCT
ATTAACCACANACCCACCCAGGTTGGGTATTATACCCCATGGTNCATAAGGACATACTATGT

SEQ ID. NO.: 74

pKVC103rB:

CGCTGCATCTTTTTCTATGCTCTCCCTGCTGGCGCTGATGGGAGATACAGACAGCAAAACGGACAGCTC
GTNTCATGATCGACTCGGACCTCTGCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGCTCACC
CGTTGNTACAAGTGTAGNCTCAAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCGN
NTGGCCCTGAGNTTCCAGAGGGNCTGGTGGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCCGN
CATGGCAGTCTTGGNCAGNAGNAANGGANTTGGNCCCAACCCCNNTGGTCCCAACCCA

SEQ ID. NO.: 75

Fig. 5K

pKVC103:

CGGCCACTGGTCATCAGATGAGCATTTTGTGTGTTTGAAGCTAGTAGCTATAGAAAAGATAGTTGTGCC
CTGATAAAGTAGCTTTTTAAAAAAGTTTGGGTTAGTTTACATTCAAGGGGCTTATGAAGAGATGCAA
GTCAGGATACATAGGCTTGATTCTTGGCAGCTTAATGAGTCTTCACGAGGCACTGAAGGTGGAAGGGTG
GAGTCCAGTAACTGCTCTGGAGCAGTGACTTCCCAATTCTGACGATCTCAACATTGTTTCTGAAGGACG
TTGCCATCTTGACACAGGAACGTGCTGTGGGGTGCCTGGCAGTGTCTGAGTAGTAGACTT

SEQ ID. NO.: 76

pKVC104rB:

CGCTGCATCTTTTTCTATGCTCTCCCTGCTGGCGCTGATGGGAGATACAGACAGCAAAACGGACAGCTC
GTTTCATGATCGACTCGGGACCTCTGTCTGCTGATGNAGGGCACCACCTACTGTTGGATTCTTATCA
GNNCAACCCGCCCNNGTGCAGATGNTAGACTCCANAAGAGNAAGNAATNAGTTGGGGNAGGTCNTTT
CCTGCTGNAGAACCTAATTCNTTGCAATTCCCC CCCC GCCCCCGG

SEQ ID. NO.: 77

pKVC107fB:

ATTACAACATCTAGAAGGCTTTCATCATACGATACAAAGCTCAGTTACAAATGTGCATCCTAGTATTTG
GAAAACTAATACCTCTCTTAATGTAACATGAAAAATTATTTCTTATGTCCTTTTTCAGGACTCCTCTT
TTATTTTTTGGTATTTTATCTTTTATGGCCACCTTGGCCTTCTGGCCAATGTGTTATGCAGTGAAAATG
CTTGTGGGCAGAGGATGCCCTACAGCGCAAAAATACCGCGCACATGGGTTTCCCAGGTA

SEQ ID. NO.: 78

pKVC107rB:

TTTTGTTTTATCCGTTTATTAGTACATGGGCGTGGGAGGATGATTTACTCATCATCTTGTATTACCAG
AGGTAGAGCATAATGCCATCTGCTAGGGATCCAGTTCGACAGCACCTCAAAACACTAGTCTGCTCACTC
ACCCTATAGGGCTTGNTCATTCCACTTGGGATGGAAGACAACAGTGCCTTTAATGCAAATGGGCCCCAG
GCAAGGAATTAACCATTTGGCTTCATGGCTCATGAAGGAATACAGNCNNATTTAANGCGNGGCAGGCAGG
AAGCCTTTGNGCTA

SEQ ID. NO.: 79

pKVC124:

CTAAAGTGGCTgAACAGTATACCCACCCCTAGCCGGCAACCTGGCTCATGCAGGAGCATCCGTAGACCT
AACTATTTTTTCACTACACCTGGCAGGTGTCTCTCAATCTTGGGTGCTATTAATTTCACTACTACTA
TTATTAATATAAAACCTCCTGCCATGTCCCAATATCAAACACCTCTATTTGTCTGATCAGTCTTAATCA
CTGCTGTCTTACTACTTCTATCACTTCCAGTCTTAGCAGCGGGAATCACTATATTATTAACAGATCGAA
ACCT

SEQ ID. NO.: 80

pKVC24B:

GCCGGGAGCCGGCCTTTGGGCGGNGGGCGGAGAGGCCCGGACGGTCGAGTGCTTCTCCTGACTGGTG
CGAGAAGAACATTTTCTATATACTTCCAGGTGCTTTTATATTCTTTTCGAGAAGAAAAATAAATTATGA
ACTCAGGATTTTGCAAGTATTCTGTGTTTCTCCTGGAGTAGGTAGTCTTCTTTTACCCAGCCACT
TTCCCTATTCTTGAAATGTGGATCTCTCTTCTCTACATGTTTTACCTCCATGATTTGGATTGGAAGG
CTGCTTTTCTTTTGGTTCCACTTTTTCAGATTCAACATAGAGAAGCTCCTAGGATGCAGTCGTCTTCTG
AAGCGCTTCCAGGGAAGAAAGAAAGAACT

Fig. 5L

SEQ ID. NO.: 81

pKVC25:

AGGTCTTAANCCCAACCCCGTCCCACCCACAGGGTNCAGCGTGGTACTACAGGCGACCCTCCCTATG
TCGGGTCTAGAACGCCCCCAGCTGGAACGAAGGGAAGAAGCTAATTACAGTGTCTTCCTTTGACTGAC
CNNCCCCCCCCCGCCCCCGCCACCAGTTCAGTCCAGGAGGGGACTTGTTAGCCCGTAGCCCATCTT
CCCCACTATCCTGGCGTGTGGGCTCGTGAATGCCTCCTAGCCAAATCACTAGAGTGCAGTGACCCAG
CCTCCTTCCTGTGCCAAGATG

SEQ ID. NO.: 82

pKVC40B:

GCAACAAGGAATGAGACCCCCAATGCCGCCTCATGGTCAGTACGGTGGTCATCATCAAGGCATGCCAGG
TTACCTTCCTGGTGTCTATGCCACCGTATGGGCAGGGACCGCCAATGGTACCCCTTACCAAGGTGGGCC
TCCTCGACCTCCGATGGGAATGAGACCTCCTGTAATGTCGCAAGGTGGCCGTTACTGATCTTACTTCAT
CCAATCTAATAGGTTTTGAGATTAAACCTTTTCTCAACTTGTGCTGGTTTATATAGCCAAGCTTCCGTC
AATAAGGCTTTATTGTTGACTTTAACAAACATTATATTACCACATACCAGGGACTATTGGACAATTATT
TTACAAGGGGAAAATT

SEQ ID. NO.: 83

pKVC43fB:

CCTGGCTGCCTGTGCCTCAACCCCACTCCCAGGGAGACCAAAAGCCTTCATACATCTAAAATTGGGGGG
GGGGGGGGGACAAAAAAGGGGGGCCACGATGGCAGACCATTTCGAAATAAAACAAAAAGACCAAGTTTT
AAGGCGAGAGTTTTAAAAAATTGGACTACATAATTTACACCAAGGCAATGTTATCACCCTGCGCCTG
TTTGGACTTGGGCGGGGACTGGCCCTTCTCCTCAGGGGGAAATGGGGTGGCTTTTGGGAAGGCAAGGGA
CTTCTGTAACAATGCATCTCAGGGTATTTGGAATGACTATTAATAAAAAAAGGGCCAATGTTACAGTC
AAGGTCCTGGGCCCA ACCTTGGAACTTTTGGGGGT

SEQ ID. NO.: 84

pKVC55B:

CCCAAACATCTACAAACACAACCTAACACCAGAAAATAAAACAAAACATTTAGTCACCTTATAAAAGTAT
AGGAGATAGAAATTTAACTTGGCGCTATAGAGAAAGTACCGCAAGGGAAAAGATGAAAGATAAAATTTAA
AGCACCACACAGCAAAGATTACCCCTTGACCTTTTGCATAATGAGTTAGCTAGAACAACCTAACAAAG
AGAACTTCAGCTAGGCCCCCCGAAACCAGACGAGCTACCCATGTACAATCTATTTAGGGGTGAAACTC
CGTCTATGTTGCAAAATTAGTGAGAAGGTTTTTGGGTAGAGGTGAAAAGCCTATCGGGCCTGGTGGTAG
CTGGTTGCCCCGAACCGGATTCTTAGTTTACCTTTTAACTTTCT

SEQ ID. NO.: 85

pKVC57B:

GCGGAAGCAGTGATCCTCCAGCCTGCAGAGGCCCCCTTCCCAGCCTGGCCCAGCTCCGGCCCCGGCCCC
GGGCTGGACTCCTCCTACACGATTTATTTGACGTTTTATTTTGGTTTCCCCACACCCCCTCAATCTGT
CGGGGAGCCCCGCCCCCTCATCTTGCTCCCTTGCCAGGAGTGAGTGACCCATGGCCTTGCGGAAATTG
TCCTCCTCTTCTCCCCTCGCACTACAGTCCTGGTCGGGGAGAGGGTGGCGGGTGCTGCTTGTTGTTTAG
TGGGTTTTGTTTGGTTTTTTGTTTTCTTCT

SEQ ID. NO.: 86

pKVC60fB:

AAAGGGTGGGGCANTTGATGCTGGTTTCTTCTCTGCGTTTTCCGTAATTCCTTCTTACTAGGGCTTTA
TAATTCTAATTTTTCTTGGTTAAGTAGTAATATAAAACACAATCAGGAACACTCTTTCTTTCCAAGTAG
GATGCAATTAGTCCAAAGTTTTTTGGATGCTGGATAAACTTGTCTTAAAGATCTCCTTCTCGTGGTCA
GTCCAAACATTCATAAACTGCCTATCTTTATAAACTTTCATAGGATCTTCCATGAGTCCATTTCATGTTG
ATGAATTTGACTCGTCTCTGTTCTGCATCAAACATCATAGGTGGGATCACAGAGAGTTGCCGCATTTGT
TTCTCATTATTTCTCCTTCTCAGAGAGCCCATCAATAATTTTCAG

SEQ ID. NO.: 87

pKVC60rB:

GTTTCCAGAAATTCGAAAACAAAGAGAACAACAAGAAAGGTTTCAGCGAGTTGGGCAGAGGGGAGCTGG
TCTTTCAGCCACGATTGCTAGGAGCGAGCATGAGATTTCTGAAATTATTGATGGGCTCTCTGAGCAGGA
GAATAATGAGAAACAAATGCGGCAACTCTCTGTGATCCACCTATGATGTTTGATGCAGAACAGAGACG
AGTCAAATTCATCAACATGAATGGACTCATGGAAGATCCTATGGAAAGTTTATAAAAGATAGGCAGTTT
ATGAATGTTTGGGACTGACCACGAGAAGGAGATCTTTAAGGACAAGTTTATCCAGCATCCAAAAAAGTT
TGGGCTAATTGCATCCTACTTGGGAAAGAAAGGGTGTTCCTGATTGTGTTTTATATTACTACTTAACCC
AGGAAAATGGGGATTATTAAGGCCTAGTAAGGAGGGATTTACGGGAAACCGCAGAGGAAGGAACCCGC
AGGCAATTGCCCCCCTTTGG

SEQ ID. NO.: 88

pKVC63B:

CCTACCCGGTTTTGGGATAATCTCACATATTGTTACCTACTATTCAGGTAAAAAAGAACCCTTTGGCTA
CATGGGAATAGTTTGAGCCATGATATCAATCGGCTTCTGGGCTTTATCGTATGAGCCCATCACATGTT
TACTGTAGGAATGGATGTAGACACACGAGCATACTTTACATCAGCCACTATAATTATTGCCATTCCTAC
CGGGGTGAAAGTATTTAGTTGACTGGCTACTCTTCATGGAGGTAATATTAAATGGTCCCTGCTATATT
ATGAGCCTTAGGCTTTTATTTTCCATTTACCGTAGGAGGGCCTAACGGGGATTGTACTAGCAAACCTCT
TCACTAGACAATGTTCTTCACGGCACATATTACGTGGGGGGCCACTGTCACTATGGCTTGTCATAGGG
GCAGTATTCGTATCATAGGGGGGTTCTGTCC

SEQ ID. NO.: 89

pKVC64B:

GCAATCCTGGCCTGGGGGCCTGAGGCCCTTCCCCTGCTCCAGGCTGTCATCTCCTGCCTCCTCTCCTCC
GGCCTCCTCAGTTTTGCCAACTGCAATTCATTTGAGTTACTGTTTATGCTAAGCATGTACTCCTGACTT
GTCACTGACTTTCCTCTGGAGCAGGTGGCTAGAAAAAGAGGCTATGGGTGGGGGAAAAAATGTTCTGT
TTCTCACTTGTAAGGCTGGTTTTTGGCTTTTCTGCCATGGGATTCTCCCCCTGACCTCTCCCCTCAGCA
ATTCTGCAAAGGGTTAAAAATTTAACTGGTTTTTNACTACTGATGGACTTAAACAACACAAAGGATG
CTGGGATGCTAACTTGGTTAACTAAACCATCAAGTTGTACCAAGTTTGGATTGGTAACTGGTNAAT
ACAAGTA

SEQ ID. NO.: 90

pKVC66B:

CGTATGAGGCAGTCCCCTGCTCGCCCCATCCCCACTGTCAGGTCTATGGGTCCGTGGGCCAGAATGGG
GTGGAATTGGGTTGAGGGAGGGACAGCCCTGGCTGACAATGATATTGGTGTAAATCAACATTAACCGAGC
CGGCTTCAGCTTACCTCAACCCGGGCAGGACACCACCACCTTGAGAAACCACAAGCTGGAGCGACCCTC
AGGCCCTGCAGGCCTTGCAAACAGCCCTGGGTGGACCCACACCAGTCCCTGTTAGCCAGCTAGGCCCA
GTCTTCCTTCAGCACCACTTTTATCCTGGGCAGGTTTCTGTGAGGTGGAAGCTGGTAAAAGCGGGTC
CCAGCCAAGGGCTTCAGGTTCAGCGCCAGCCAGTAACCTCAATTCTTAACGGTGGGCAGGA

SEQ ID. NO.: 91

pKVC82B:

GCCACCTGACCCTCCTAACCCATGGCTGTCTGATGATACTACTTTCTGGGAACCTGNAAGCAAGCAAAG
AACCAAGTCAGCAGAGGGTAAAACGATGGGGTTTTGGCATGGATGAAGCATTGAAAGACCCAGTTGGGA
GAGAACAGTTTCTTAAATTTCTAGAGTCAGAAATTCAGCTCAGAAAATTTAAGATTCTGGCTAGNCAGTG
GAAGNACCTGAAAGNAAAAGGTCTAATNAGGAGAAAAGTTCCTTTCCCGGAGATTCAGGGAAAATATGG
GCAAAGNAATTTTCTTGGGCTCCCTGGGAGGCTTCCCAGNTGCCAATCCAAACCTTGGGGTTTTCT
NAAGGAGGCTNATGGATT

SEQ ID. NO.: 92

pKVC110

GAGAAAGACATAATGGTTATGGCATTGGCTTGAAACCAGTTAAAGAGGGTTCGATTCCTTCTTTCTTA
TTTTAATAGTACGTAAGTTGGCTCTTCAAATGTGTGGTACGGAGGAGGACATCCATGCAATCATTCAAG
ATTAGTTGTGGTTAATTCTACTATGGCCACTTCTCGCTTGGA TGGCAAAGCTTCT

SEQ ID. NO.: 93

pKVC134: Homologous to human alpha tubulin; Accession HSHA44G

CCGCCAGTGTGCTCTAAAGTGTGGTACCCTGGTGGAGACCTGGCCAAAGTACAG
CGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGC
CTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGCCTTTGTTCACTGGTATGTGGGTGAGGGCATG
GAGGAAGGAGAGTTTTCTGAGGCCCGTGAGACATGGCTGCCCGTGAGACATGGCTGCCCTTGAGAAGGA
TTATAGGAGGTTGGTGTGGA

SEQ ID. NO.: 94

pKVC108: Homologous to Mouse Initiation factor eIF-4A;

Accession MMEIF4AL

TCTTCTCCCAAAAACACTAATCCATGTCCGTAACCCACTCAGCCTCCAGACCCAGAGGCTCTCCCCCA
CCCAGCTGCCACCTCTAAAGAGGATTCAAGGGGCTATAGTGTACCCAACCTCATTTGCTGGACCAAA
TCTGGAGAACCCTTGAGCTAGGTGGCCcATGGGgTTGTCCcAGGTGGGGgAGCAGGGGAGAGAAAATG
GTAGCCATTTTTACATTGTTTTGTATAGTATTT ATTGATTCAGG

SEQ ID. NO.: 95

pKVC105B: Homologous to Human mRNA for prolif. associated protein;

Accession HSPAG

GTCAGACACAACCTTTCTGAATCCTCTNAGGANGGTGATCCAGTTCATGAANATTCTCTGTAAAATNANT
NTGGNAACTANATNAGTGNGATNCAGGTCTNGAGNNTCTCCTTCCAGTGNCTAAAAAGTNCACAGAN
GNCAGGAACNCCTATCTGCATGCAGTCACCAGTTCTCATNC TCTANGCA

SEQ ID. NO.: 96

pKVC92B: Human Mitochondrial hinge protein; Accession HSHINGE

CCCAGCCTTCATGAGCTGGTCATCAGGATACTTTCTTATGGGNTNGANCATGCCANTTGCTTNTNCGNG
TANATGTAAGTTCATGNCAACCNCATTTTTTTTTCTAGCCTNNGGCTNAAGGTNANTCGTCTCNTTANG
CAGCNGANNCAGTTGNAGTCTNTCAAANGNNCACAAANACCTAA

SEQ ID. NO.: 97

pKVC91: Homologous to Bovine NADH dehydrogenase; Accession MIBTX

GGGTAAAGTGATAGGAGGAGAAGGGCTGAGTAGGTGGAGGgCTATTAGGGCATTCTCGGTGTAAATG
ATGGGTTGATATTTTAAATGTGGTGTGTGATTTGCCTCGTTGAGTTATAATAAGTATGTAGAGggaGT
ATaGccCTGTAATGATGATATTAGTACCCATTAGGATAATGGTTATGTTTGATCATGAGAAGGAGGCTA
TTACTAC

SEQ ID. NO.: 98

pKVC90: Homologous to Human hnRNP core protein A1; Accession HSRNPA1

ACAACCTTTGGCCGTGGAGGAACTTCAGTGGGCGAGGTGGCTTTGGCGGCAGTCGAGGTGGTGGTGGAT
ATGGTGGCAGTGGGGATGGCTATAACGGATTTGGTAACGATGGAAGCAACTTTGGAGGTGGTGGAAAGCT
ATAATGATTTTGGCAATTACAACAATCAATCTTCAAATTTTGGACCCATGAAAGGAGGAAATTTTGGAG
GCAGAAGCTCTGGCCCCATGGTGGTGGAGGCCAATACTTT

SEQ ID. NO.: 99

pKVC86B: Homologous to Rat Ribosomal protein S27; Accession RRS27

GCGAAGGACCTCCTGCACACGTCCCGGAAGAGGAGAAGAGGAAGCACAGAAGAAGCGCCTGGTGCAG
AGCCCCAACTCCTACTTCATGGACGTGAAGTGCCCGGGTGCTACAAAATCACCACCGTGTTTCCCT

SEQ ID. NO.: 100

pKVC82: Human Carboxypeptidase E; Accession HSCARBE

ATCTGCCATTTTAGACTTAAAGGAAATATTCCACGTGTTATTTACGATCCAGAAGTTTTTGAGTAATTC
TGGCTTTTAAAACTAATGAAGTCCTTTTAGTGTAATGGTAACAGTGCCACATAGTGAATGCCACTGAA
AAGGTCAACAGCTACATTTTGGTGTTGTGAGCATTATACCGCAAGACTTACATAGTTCAGTATAA

SEQ ID. NO.: 101

pKVC80: Homologous to Rat VAMP-2; Accession RNVAMPB

GGTCCTTGATCACTTTTCATTTGCATGACGTTCCCTTGACAGGTGGTGGGAGCCTGGGCTTTTGGGGAGCC
AGAACCTTCTGGCCCCAGAATCACCCCTCCTAGCCCCCTCTAGTCCAGTTTGCCTCCCTGCCCCCA
TTTTCAAACCTCTTGTCCTCCCTCCCTCCCCCTCCCCCAGCTGGTGTGGAAGTGTCTCGGAG
TTCAGTGTGTATGAAGGACAATAGTTTGCCTGGAGTTT

SEQ ID. NO.: 102

pKVC79: Homologous to Bovine Nuclear encoded ADP/ATP transporter;

Accession BTADTPMT

GGATGATTGCCAGAGCGTGACAGCGGTGCGAGGGCTGGTGTCTACCCCTTTGACACTGTCCGCCGTA
GATGATGATGCAGTCTGGCCGGAAGGGGCGGATATTATGTACACTGGGACGGTGGACTGCTGGAGGAA
GATTGCAAAAGATGAGGGAGCCAAGGCTTTCTTCAAAGGTGCCTGGTCCAATGTGTTGAGAGGCATGGG
CGGAGCTTTCGTATTGG

SEQ ID. NO.: 103

pKVC59B: Homologous to Rat scg10; Accession SCG1_RAT

ACGACTCACTATCAGGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCAGTGTGGGAAAAGG
AGAGGCATGCCGCGGAGGTGCGCAGGAACAAGGAAGTCCAGGTTGAACTGTCTGGCTGAAACGATGGAG
GGTATGGCACGCCACCATTAGTAAATCCCCCTGCCTATATTATAATGGTTCATGCGATATCAGTATG
GGAAATGTATGACATGGTTTAAAAAGAACTCATTATAAAAAACAAAAACAAAAACAGAATC

SEQ ID. NO.: 104

pKVC55: Homologous to Human LAMP-1; Accession HSLAMP1A

AGCATGCTGATCCCCATTGCCGTGGGcGgCCTGCGGGGGCTGGTCCTCATCGTCCTCATTGCCTACCTC
ATCGGCAGGAAGAGGAGCCACGCGGTACCAGACGATCTAGCAGGGCTGCGACACGTCGGGCCGGCTGC
CACTTCCGGTCTCCGCTCGTCCCCTGAGCTTAGGTTGGCGTGGAGGGCGGCACGTTTCTTGCAAACCTG
ATTTTCAAATCTGCTTTATCCGATGTGAAGTTCATCTTGCAACATTTACTATGCACAAGAGTATTGAAA
TGAC

SEQ ID. NO.: 105

pKVC49B: Homologous to Chicken Contactin; Accession GGCONTAC

TTCATTATGAAAATATCAATAAATATGTCATTAGTTTACATTCAACTCTTTGTTATAAAATTAACCTT
TTAATAATAAGTGAAATGGGTGATTTCCCCCTGGAGGGATGTCAACAGGCTTAAATCATTTCCCGGT
TCATAAAATACAACTCCTTTGAAAAAGGGACAAATCTCTTCATACTTTTGGGGAACGATACTGTGT
AAGCCCTCTGTACAAAAGTTTGGGGTTTTCATTGTTACACTTTGGGGTTTCCCTTTTCAAGGGGCCCC
CCTGTGGGGGGTTTTTTTTTATGCGGGCAACCACTAAATTTTTTTTCCCAAATGGAATGCCCGCCC
TTTTTTTTCTAATGTTTTTTGCAATAAGGGGGGCCAAACCGGGGGAGGGTTTTTCATGAAAAGGGT
TCCTTAAGGGTGAGGGGAACACGCTTTGGGGGGGGTTTTCTTTTAAGTTTGTGGCCCCAGTAGGG
GGGAGAAAGCCCTCCCCCGGGAAACCAGGGTTTGGTTCCCCACGG

SEQ ID. NO.: 106

pKVC47B: Homologous to Human 71 kD heat shock cognate protein;

Accession HSHSC70

CCTGAGAATAGGTCTAGCATTGTTCCACACAAAACATTTGAAGGACCCAAATTTGTAGCAAATTCATG
GCAGTGAAGTTGAGCTGCTATAGTTAATAAACTGGGCATTCTTGATACTTGAATATGGAATATGTGCAC
AAGGGAAGTAAATACAACATTGCACTTTATAAGCACTGTATTGTTAAGTGGGAAATGCAATGTCTTTAA
AATAAACTGTATTTAAAATTGGCGCCCCAAAA AAAAA

SEQ ID. NO.: 107

pKVC46B: Homologous to Human 71 kD heat shock cognate protein;

Accession HSHSC70

CCTGAGAATAGGTCTAGCATTGTTCCACACAAAACATTTGAAGGACCCAAATTTGTAGCAAATTCATG
GCAGTGAAGTTGAGCTGCTATAGTTAATAAACTGGGCATTCTTGATACTTGAATATGGAATATGTGCAC
AAGGAAAGTAAATACAACATTGCACTTTATAAGCACTGGTATTGTTAAGTGGGGAATGCAATGTGCTTA
AATAAACTGTATTTAAAATTGGCACCAA

SEQ ID. NO.: 108

pKVC35B: Homologous to Human Vacuolar proton ATPase channel;

Accession HSPCHSUA

CTTTAGAGGACACACACNCACGGGGCCGCCGCCCCCAGTAGTCGGTCTTGTAATGCGCAGTGTCTTA
GTGCCCCGTTGTCTGCTACCCCGGCCTCGCCCCGCCCCGCCCCGTGCCGTGGACATCCGGGGCCACTCC
TTACCCATCCGGGCCTCCGGCCCCACTCATCTGCCCTAGAGCGCTCTGTAGAAGGGTGAATTAGAGTT
GTATTTCTCTTCACTGGATGTTTCTTATTTATA AAGATTTGATCTGTTC

SEQ ID. NO.: 109

pKVC27B: Homologous to Rat Cytoplasmic Succinyl CoA synthetase;

Accession RNGLTA

GCGACACGTTCTGTCATTTATGTTCTCCTCCTTTTGCTGCTGCTGCCATCAATGAAGCTGTTGAGGCG
GAAATGCCCTTGTTGTGTGCATTACTGAAGGTATCCACAGCAGGACATGGTGCGGGTCAAGCACAAA
CTGCTGCGTCAGGGAAGACCAGGCTGATCGGGCCTAACTGCCCTGGAGTGATCAATCCTGGAGAATGC
AAAATTGGCATCATGCTGGCCATATTCACAAGAAAGGAAGAGTTGGTATTGTGTCCAGATCTGGG

SEQ ID. NO.: 110

pKVC22: Homologous to Human clq beta isoform; Accession HSC1QBR

GGAAAGATGGGATTGTATGAAACACTGCATTTTCACAGCAAAGACCTCAGTCCAGAACACAACACAGGGG
ACCAAGTGGATTGAGGTGTGGTCAAACTCTGGGGATCACAGTGGGGATACCACCTCCAGGGCTGGTGA
CAGATTCAGGACCCTCCTGGCACACCCGGGACCCAGGGATAAAAGGAGAGAAAGGGCTGCCAGGGCTG
GCTGGAGACCATGGCGAGTTTGGGGAGAAGGGA GACCAGGGATTCTGGAATCAGAAA

SEQ ID. NO.: 111

pKVC22B: Homologous to Human Phospholipase A2; Accession HUMPHLA2

TTCCAGACGGGAGATTGATTGGAAAAAAGTAATGTGTTCCATTTAAATTTTGGTATATGGCATTTT
CTGACTTAGGAAGCCACAATGTTTTTGTCTTGCCCATCATGACATTGGGTAGCATTAAGTTTTGTGC
TTCCAAATCACTTTTGTGTTTAAAGGATTTCTTGATCTTGTTATAGCCTGCCTTCAATTTTGATCTTTAT
TCTTTCTATTTGTCAGGTGTACAGGATTACCTT TTTTAGCCTTCTGTCTT

Fig. 5R

SEQ ID. NO.: 112

pKVC21: Homologous to Xenopus nrp-1b; Accession XLNRP

ACCCTTTCCTATGTGTTTTATCTAATTATTTTGGTTGTTAATATGGTAATAATTAAAAGTCAAGGTAAA
TTTTAAATATTAAGATTTCTGATTTATTGAGCTTGACTTATGCCACCACGCTTATGTAAAATGAAAGTA
GCACCATGGTGAAACTGAAAAAAGTTGCTCAGTTGTAACAGTTTTGATTTATTCTTTCTTGACCTCT
TTCCCTTATTGTCTTGAACCATAGCAAAAGGATACTGCATCTCTTAATAATTGTAGTGCTGAGGTTATT
GAaGTTATAT

SEQ ID. NO.: 113

pKVC18: Homologous to Human Cytochrome oxidase I; Accession MIHSCG

GTTATATTGACTCCTACAAACATAATCGTAAAGTGAATCTTTGCTCAAGTGTTGTCAAGGGTATATCCT
GAGAATAGGGGAATCAATGGACGAAGCCTCCTATGATAGCGAATACTGCTCCTATTGACAAGACATAG
TGAAAGTGGGCCACTACGTAATATGTGTCGTGAAGAACAATG TCTAGTGAAGAGTTTGCTAGTACA

SEQ ID. NO.: 114

pKVC17B: Homologous to Rat SubstanceP receptor; Accession RNSPR05

GCTATAGACACACAACTTTCACT
CACCA

SEQ ID. NO.: 115

pKVC12B: Homologous to Human 90 kD heat shock protein;

Accession HSHSP90R

ACGCTCGTTTTCCAAAGAGAAGAGCGTTGTTTAGAGTAGCGAAATTCGAAGGCTGCTTAGGCGCATTGT
AAAGCTGTTGGGGAAATAACTCCACAAGTTTCGTGAGTGGAAATGTAGTGCTCGAAACACATTCTGCTT
TAAAAGGTTGTAACAAATACAAACAAATTTAAAAAAGCTCTGACAAATGTTTTGTGTGGGGAAGCGGG
GTTCCAAAATACAGGGCGGCCCC

SEQ ID. NO.: 116

pKVC10B: Homologous to Human Cytoskeletal gamma actin;

Accession HSACTCGR

TTGTCATCTCTTCAAGAATTGACAACAGATTTTGGTTTTCTACTGTCATGTGGAACATT
AGGCCCCAGCTTCGGCTCCTTGTCGAGGAAAATAAA

SEQ ID. NO.: 117

pKVC9: Homologous to Human v-fos transformation effector; Accession HSFTE1A

GCATCTGATGGCCTTAAGGGTCGTGTGTTTGAAGTAAGCCTGGCTGATTTGCAGAATGATGAAGTTGCA
TTTAGGAAATTCAAGCTAATTACTGAAGATGTTTCAGGGCAAAAACTGCCTGACTAATCTCCATGGCATG
GATCTTACCCGGGACAAAATGTGCTCCATGGTCAAAAAATGGCAGACCATGATTGAAGCTCACGTTGAT
GTCAAACTACCGATGGGTATTTGCTTCGTCTCTTTTGTGTCGGTTTTACTAAAAAACGCAACAATCAG
A

SEQ ID. NO.: 118

pKVC6B: Homologous to Chicken Amphiphysin; Accession GDAMPHIP

CCTTCCAGAACCCTGAGGAGCAGGATGAAGGCTGGCTCATGGGCGTGAAGGAGAGTGACTGGAACCAGC
ACCTAGAGCTGGAGAAATGTCGGGGCGTCTTCCCCGAGAACTTCACCGAGCGGGTTCAGTGAGGGCAGC
AGCTGCTGAG

SEQ ID. NO.: 119

pKVC6: Homologous to Human TAPA-1; Accession HSTAPA1

TCTACGACCAGGCTTTGCAGCAGGCCGTGGTAGACGACGACGCCAACAAATGCCAAGGCCGTGGTGAAGA
CCTTCCATGAGACGCTCAACTGCTGTGGCTCCAGCACGCTCTCCGCGCTGACCACCTCCATTCTCAAGA
ACAACCTGTGTCTTCAGGCAGCACTGTCATCAGCAACTTCTTCAAGGAGGACTGCCACCAGAAGATCG
ATGACCTCTTCTCGGGAAAGCTGTATCTCATTG GCAT

SEQ ID. NO.: 120

pKVC4B: Homologous to Rat alpha internexin; Accession#RNINTLAA

CACCTAAAGAGTTGCCAGGTCTCTGTACACATCTCCATTCAACAGATAGGGTGTGATGCTTTTACT
AACTTTCTTATCCTAGGACCTGCTGCAATGGTTCAAGGAACTGGAAAGATGCTTTCTTCTTCTCTT
CCCTCACTCCATCCCTGTCTTTACTCCTCAGACTTCTGTAAAAACATTAGTAAGATAAGAATTAAGT
CACACGAATCCAC

SEQ. ID. NO.: 121

>pKVC154

ATTTGGCTCAGTGGCAGAGCGCTTGCTAGGAAGAGCAAGGCCCTGGGTTCGGTCCCCAGCTCCGpoly
(A)

SEQ. ID. NO.: 122

>pKVC159

GGGAGGAGGAGGAAGAGGAGGAAGGAGAGGAGGAGGAGGAGGCTGCAAAGGCTCTGGGCTCCTCTpoly
(A)

SEQ. ID. NO.: 123

>pKVC151

GTAATTATTGGCTCAACTTTCTAATTGTCTGTCTACTACGACAACTAAAATTCCACTTCACATCAAAA
CATCATTTTCGGATTTGAAGCCGCAGCATGATACTGACACTTCGTAGATGTAGTTTGACTATTCCTATAC
GTTTCTATCTATTGATGAGGATCCTpoly(A)

Fig. 5T

SEQ. ID. NO.: 124

>pKVC158

GATTTGGAGAAGCCTTCGCATCAAAACGAGAAGTACGCTCAATTTCTACTCTCAACTAACCTAGAAT
GACTGCATGGATGCCCCCACCCTACCACACATTCGAAGAACCCTTCTACGTAAAAGTTAAATAAGAAA
GGAAGGATTGAACCCCTACAACCTGGTTTCAAGCCAATTCATAACCATTATGTCTTTCTCAATpoly
(A)

SEQ. ID. NO.: 125

>pKVC160

AAGGATAATGCTGTTTATTAATAAATACTCAGGAAGTCAGGGTATTGATGCAATTTTACATACGCACT
TGGGTAGTCTGAAGTTCCATTATTCCAGCAGTTTATATAAATGTTTCAGATCAAAGAGAAAAGAAAACA
CTTTACAGAGACCAGCAGTTGCTTATCAGTTTGGTCATGAGTCTGCTTGTAGTAAAAATAAACTCCCT
CTTGCAATTGCTGAAGAATGTCCTT

SEQ. ID. NO.: 126

>pKVC157

CAGCTCCCTAGTACTTTACTATTATTTCACTAATACTAACAACAAAATAACACACACAAGCACAATAG
ACGCCAAGAAGTAGAAACAATTTGAACAATCCTCCAGCTGTCATTCTTATCCTAATTGCCCTTCCCT
CCCTACGAATTCTATACATAATAGACGAGATTAATAACCCAGTTCTAACAGTAAAACTATAGGACACC
AATGATACTGAAGCTATGAATATCTGACTATAAGACCTATGCTTTGACTCCTACATAATCCC

SEQ. ID. NO.: 127

>pKVC156

CCATGCTTGTGACAGACATACAGCCACTTCCAATAAGCAAGCCTCTGCTTCTGCTACCTGCATGGA
GCCCACTGTGACACTCAGACCATCCCCGGTCACTCACTCGTGTCTGAGAATCTCAGTGAGAGCTGCCTC
TGTCACGGACGGAAGCCAACACAGCCACCTCTCGACCTGGCTCCCCACAGCACCCACCCTCCCTGCATG
CAGCTGTCCCTGCTAACCCCCAATGTTATGTTACACTGTGTAATCCCCACTGCTGCCGTGTGTGGGTT
GTGTACGTCGTCATGTCCTGGTTTATACTATGGTGCGGTGGGAAGGATTCTGTAATGCTGCTCTAA
GA

SEQ. ID. NO.: 128

>pKVC153

CCTAGACTCACAAGTCAAAGTAATACTAATATCTTATTGACCCAATTATTGATCAACGGACCAAGTTAC
CCTAGGGATAACAGCGCAATCCTATTTAAGAGTTCATATCGACAATTAGGGTTTACGACCTCGATGTTG
GATCAGGACATCCCAATGGTGCAGAAGCTATTAATGGTTCGTTTGTTCACGATTAAAGTCCTACGTGA
TCTGAGTTCAGACCGGAGCAATCCAGGTCGGTTTCTATCTATTTACAATTTCTCCAGTACGAAAGGAC
AAGAGAAATGGAGCCTCCTTACCATAAGTGCTCCCAACCAATTTATGpoly(A)

SEQ. ID. NO.: 129

>pKVC152

GCTTCAATTTACTAGTTCAACTTATATAAAAAACAACCTAATGGGCTAAAACAAAATAAATATGAACTAA
AAAATTTGGTTGGGGTGACCTCGGAGAATAAAAAATCCTCCGAATGATTTTAACTAGACTCACAAGT
CAAAGTAATACTAATATCTTATTGACCCAATTATTGATCAACGGACCAAGTTACCCTAGGGATAACAGC
GCAATCCTATTTAAGAGTTCATATCGACAATTAGGGCCACGACCTCGATGTTGGATCAGGACATCCCA
ATGGTGCAGAAGCTATTAATGGTTCGTTTGTTCACGATTAAAGTCCTACGTGATCTGA

Fig. 5U

SEQ. ID. NO.: 130

>pKVC161

AGAGATATCGGAACCCTCTACCTATTATTTGGAGCCTGAGCAGGAATAGTAGGGACAGCTTTAAGTATT
CTAATTCGAGCTGAACTAGGACAGCCAGGCGCACTCCTAGGAGATGACCAAATCTATAATGTCATCGTC
ACAGCCCATGCATTGTAATAATTTCTTTATAGTAATACCTATAATAATTGGAGGCTTCGGGAAGTGA
CTTGTAACCTAATAATTGGAGCCCTGATATAGCATTCCACGAATAAATAACATAAGCTTTTGACTG
CTTCCTCCATCATTTCTACTCC

SEQ. ID. NO.: 131

>pKVC162

GAGCTGTTGCCAGTGTAAGACAGCAAACATGGACACTCTCGCACTGTGCATCACAAAGCTAACAAATC
GAAATCTTGAATGCAGTCTGTCTAAGTCCAGGCAAGTGACAGCCATGTGTGTCTGCAGTGCTGTGTCA
CCACGTCTGCATTGTTGGAGCTGCTGCAGGGACACTGAGATGAGCAGGTTCTTTGGAAAGAACTGTTG
TGCTCCTCAAAGCAGTGTTTCAATTTTAAAGGTTCTTAGCCCTCAGTTCCTTATGTGGAAGTGTAGG
ATCCCCTTCATAAATTTTAAAGTGCTTATGTGATCCAATTGGTCTACATTTT

SEQ. ID. NO.: 132

>pKVC36BR

CTTTAGAGAAGGCAGGTCTTACAAACACTACAGAAAAGCCGTTTGGACGTAA
AAATCCAAGGAGAAAGGAGTCATTAGGAAATGTAACATAGGACACAGAACG
CATGTTGTGTGATGGTCCCTTCTCTTCCGTGTGGTTCCAGAATATGCTCCTGAC
CCCAGAGCCGCCACCTGAGCGCGCACCGGGAAGGTCACAGACGACTTCAGGC
TTCAGGCGCAACGTC